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Welch, Rodney A.
Burland, Valerie D.

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 <211> 1749
 <212> DNA
 <213> Escherichia coli

<400> 32
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 <211> 1962
 <212> DNA
 <213> Escherichia coli

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<210> 34
 <211> 282
 <212> DNA
 <213> Escherichia coli

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<210> 35
<211> 5225
<212> DNA
<213> Escherichia coli

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<222> (377)..(377)
<223> Unsure

<220>
<221> misc_feature
<222> (1204)..(1204)
<223> Unsure

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<210> 36
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<210> 37
 <211> 108
 <212> DNA
 <213> Escherichia coli

<400> 37
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<210> 38
 <211> 221
 <212> DNA
 <213> Escherichia coli

<400> 38
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<210> 39
 <211> 11366
 <212> DNA
 <213> Escherichia coli

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<222> (743)..(743)
<223> Unsure

<220>
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<223> Unsure

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<211> 421
 <212> DNA
 <213> Escherichia coli

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<210> 42
 <211> 65
 <212> DNA
 <213> Escherichia coli

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<210> 43
 <211> 3281
 <212> DNA
 <213> Escherichia coli

<400> 43
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 <211> 498
 <212> DNA
 <213> Escherichia coli

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<210> 46
 <211> 6277
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc feature
 <222> (2284)..(2284)
 <223> Unsure

<400> 46
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cgcacagagt gctggcatca cattctgtgc gtatggt	6277

<210> 47
 <211> 57
 <212> DNA
 <213> Escherichia coli

<400> 47	
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<210> 48
 <211> 4777
 <212> DNA
 <213> Escherichia coli

<400> 48	
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 <211> 981
 <212> DNA
 <213> Escherichia coli

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<210> 50
 <211> 4136
 <212> DNA
 <213> Escherichia coli

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<210> 51
 <211> 492
 <212> DNA
 <213> Escherichia coli

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193

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<211> 88
<212> DNA
<213> Escherichia coli

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<211> 5203
<212> DNA
<213> Escherichia coli

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 <211> 170
 <212> DNA
 <213> Escherichia coli

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 agaatatccc atcacagata aaataaatat gtgcatggta gtcttgaatc 170

<210> 70
 <211> 773
 <212> DNA
 <213> Escherichia coli

<400> 70
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 <211> 713
 <212> DNA
 <213> Escherichia coli

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 cttgcagttg ccagaccgca aggtgtttta acaaatacaa aggggtttta ataactggct 660
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<210> 72
 <211> 348
 <212> DNA
 <213> Escherichia coli

<400> 72
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<210> 73
 <211> 332
 <212> DNA
 <213> Escherichia coli

<400> 73
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<210> 78
 <211> 144
 <212> DNA
 <213> Escherichia coli

<400> 78
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 gttttgtgaa ttgtccagat cttt 144

<210> 79
 <211> 92
 <212> DNA
 <213> Escherichia coli

<400> 79
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 ggcgtcacat caggcaacgg ctgtcggatg ca 92

<210> 80
 <211> 182
 <212> DNA
 <213> Escherichia coli

<400> 80
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<210> 81
 <211> 1701
 <212> DNA
 <213> Escherichia coli

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<210> 83
 <211> 532
 <212> DNA
 <213> Escherichia coli

<400> 83	
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<210> 84
 <211> 70
 <212> DNA
 <213> Escherichia coli

<400> 84	
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<210> 85
 <211> 12290
 <212> DNA
 <213> Escherichia coli

<220>
 <221> gene
 <222> (1009)..(1884)
 <223> The complementary sequence is the coding sequence.

<220>
 <221> gene
 <222> (1797)..(5606)
 <223> The complementary sequence is the coding sequence.

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<211> 5999

<212> DNA

<213> Escherichia coli

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gtgtatagat tatgtсatcc atc 143

<210> 122
<211> 53
<212> DNA
<213> Escherichia coli

<400> 122
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<212> DNA
<213> Escherichia coli

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<211> 1346
<212> DNA
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128

<210> 126

<211> 452

<212> DNA

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<400> 126

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tgctttttca gaatctgtcc attcgtggtc ag 452

<210> 127

<211> 82

<212> DNA

<213> Escherichia coli

<400> 127

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gtttgccgcc atagtgcgt ac 82

<210> 128

<211> 69

<212> DNA

<213> Escherichia coli

<400> 128

gtaagtctct tgtgccattc cacctcatatc aggtttgcct gcaaacagta ctgatattgc 60

actgccaga 69

<210> 129

<211> 120

<212> DNA

<213> Escherichia coli

<400> 129

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<210> 130
 <211> 174
 <212> DNA
 <213> Escherichia coli

<400> 130
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 tttgattagg aaagtgaaaa ggaaaggagc aagctaagtt gctcccttta atca 174

<210> 131
 <211> 82
 <212> DNA
 <213> Escherichia coli

<400> 131
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 <211> 81
 <212> DNA
 <213> Escherichia coli

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2147

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727
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138
58
DNA
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139

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<211> 1261
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<213> Escherichia coli

<400> 151

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ccacatgatt tatttgatat ttattaccaa tagatgcata cgaaccacaa cctcagaga 1140
tcaaaccttg tattttccct ttaattgata agtatatcat atttgacata tatattctcc 1200
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<211> 7306

<212> DNA

<213> Escherichia coli

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aaaaagccaa	acgaccaatg	ctatccgcc	gaataactaa	caacgcccc	gataccgcgc	2040
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 <213> Escherichia coli

<400> 153
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<211> 5481
<212> DNA
<213> Escherichia coli

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THE UNIVERSITY OF CHICAGO

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 <211> 306
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 <212> DNA
 <213> Escherichia coli

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 <213> Escherichia coli

<220>
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5489

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<211> 24328

<212> DNA

<213> Escherichia coli

<400> 213

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<212> DNA
<213> Escherichia coli

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<210> 219
<211> 102
<212> DNA
<213> Escherichia coli

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<211> 14518
<212> DNA
<213> Escherichia coli

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<223> Unsure

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<220>
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<222> (10834)..(10834)
<223> Unsure

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<210> 222

<211> 52

<212> DNA

<213> Escherichia coli

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<211> 445

<212> DNA

<213> Escherichia coli

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<211> 2408

<212> DNA

<213> Escherichia coli

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<210> 226
<211> 114
<212> DNA
<213> Escherichia coli

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<210> 227
<211> 5353
<212> DNA
<213> Escherichia coli

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<212> DNA
<213> Escherichia coli

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aagtcataa 69

<210> 229
<211> 54
<212> DNA
<213> Escherichia coli

<400> 229
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<210> 230
<211> 710
<212> DNA
<213> Escherichia coli

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<210> 231
<211> 713
<212> DNA
<213> Escherichia coli

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 <212> DNA
 <213> Escherichia coli

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<210> 233
 <211> 711
 <212> DNA
 <213> Escherichia coli

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<210> 235
 <211> 202
 <212> DNA
 <213> Escherichia coli

<400> 235	
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gccacaatta aagaaaatcc tgcctttttc cgggaacttg cttoccatta atcatttaac	180
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<210> 236
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<212> DNA
<213> Escherichia coli

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<212> DNA
<213> Escherichia coli

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<210> 238
<211> 3999
<212> DNA
<213> Escherichia coli

<400> 238
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3999

<210> 239

<211> 52

<212> DNA

<213> Escherichia coli

<400> 239

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52

<210> 240

<211> 425

<212> DNA

<213> Escherichia coli

<400> 240

ctctaataat aaaacaagga agtgttctat gacgtatgga gaagcgtatc tggaagggtg

60

gaaaaacatc ttttaattatg aaggtgtttc caatcgcttc gagttctggt cgtttatgat

120

tggtagtggc gttatctgtc tgcttccgct tttatgttgg tggttagcgg taacaattaa

180

caatgactat ggtgttttca ttttttttgc gctgcccgct tcatttattt taacgttgat

240

ttttgccgta ccggcgatag cgtagccgt cagaaggatg cacgatatcg gatattcagg

300

gtgggtgggtt accattgccg tgttgatccc tggtacgggc gtaattctgc ttatactgtg

360

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420

ctgcg

425

<210> 241

<211> 635

<212> DNA

<213> Escherichia coli

<400> 241

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acaggagcac gagatcatga ctgcaaaacg taccacacaa agtgtgaccg tcaccgtcga

120

ccgtgagtta gtcaatcgcg ctcgatgatgc aggcctaaat atgagcgcca cccttacggt

180

tgcgctcaat gctgaactta aaaaacatgc agcaacacgt tggcgtgaag agaacgcaga

240

agotatcgct gcgttaaato aattggctga tgaaaccgga tgtttctctg atgagtaccg

300

gagcttctag cgatgcaatt tacgggtatac cgcagtcgcy gcaggaacgc cgcgtttccc

360

tttgttattg atgttaccag cgacattatt ggtgagatta atcgccgtat cgttattcca

420

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480

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540

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600

ttagattttta tgctcgacgg gatttaagac gctac 635

<210> 242
<211> 119
<212> DNA
<213> Escherichia coli

<400> 242
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aattgccgga tgcggcgtga acgccttctc cggcctaccg aacttcgcca gcgtgacta 119

<210> 243
<211> 1827
<212> DNA
<213> Escherichia coli

<400> 243
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gttattttata tttttcacgg gggattaatt ttagttattt ttagttgaat cgttttacct 120
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tttttcttta ttgatattat ttgtatacgt ttttttttga ggggagattg tgatgagcaa 540
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cgaagagtta ggttggtatcg atttggggca tgctcaggga caagatgcca gaatattaaa 660
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<210> 244
 <211> 712
 <212> DNA
 <213> Escherichia coli

<400> 244	
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aaacaagaaa	tcaaaagggg gtcccaatgg ggaacgaaaa gagcttagcg cacacccgat 180
ggaactgtaa	atatcacata gtttttgcg caaaataccg aagacaggtg ttctacagag 240
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agtaacgaag	ttggatgcaa atgtcagatc gtgtgogcct gttagggcgc ggctggtaag 660
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<210> 245
 <211> 711
 <212> DNA
 <213> Escherichia coli

<400> 245
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 gtaacgaagt tggatgcaaa tgtcagatcg tgtgcgcctg ttagggcgcg gctggtaaga 660
 gagccttata ggcgcatttg aaaaacctcc ggctatgccg gaggatattt a 711

<210> 246
 <211> 711
 <212> DNA
 <213> Escherichia coli

<400> 246
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 caagaaatca aaaggggggc ccaatgggga acgaaaagag cttagcgcac acccgatgga 180
 actgtaaata tcacatagtt tttgcgcaa aataccgaag acaggtgttc tacagagaga 240
 agcgtagagc aataggcagt attttgagaa agctgtgtga gtggaaaagc gtacggattc 300
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 aacgaagttg gatgcaaatg tcagatcggtg tgcgcctgtt agggcgcggc tggtaagaga 660
 gccttatagg cgcatttgaa aaacctccgg ctatgcgga ggatatttat t 711

<210> 247
 <211> 711
 <212> DNA

<213> Escherichia coli

<400> 247

gtgcacagaa aacccccagc taggctgggg gttccgga aa gctttcagct ttgagccagt 60
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caagaaatca aaaggggggc ccaatgggga acgaaaagag cttagcgcac acccgatgga 180
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aacgaagttg gatgcaa atg tcagatcgtg tgcgcctgtt agggcgcggc tggtaagaga 660
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<210> 248

<211> 746

<212> DNA

<213> Escherichia coli

<400> 248

gtgcacagaa aacccccagc taggctgggg gttccgga aa gctttcagct ttgagccagt 60
tattaaaacc ccttttgatt tgttaaaaca ctttgcggtc tggcaactgc aagtgtcaaa 120
caagaaatca aaaggggggc ccaatgggga acgaaaagag cttagcgcac acccgatgga 180
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gccttatagg cgcatttgaa aaacctccgg ctatgccgga ggatatttat totttttggc 720
gattgagtgc cggacggtgt acaaac 746

<210> 249
 <211> 1463
 <212> DNA
 <213> Escherichia coli

<400> 249
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 tctacggcaa aactctttca actttctcac accagcctct cactctggat taatcttttt 180
 cttcttcacg gtcctcgggc actggattgc agacacaagc gtagctattc tcctgaagat 240
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 caaaaagccg gttaactgaa actgtccagg ttttgggggt cagttcatgg cgcgttttat 1440
 caggccagcg tcgcatcaga tag 1463

<210> 250
 <211> 3221

<212> DNA
<213> Escherichia coli

<400> 250
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tttcaactat cacaagataa tggatatatgc gogagaatgc acctgcttta tgtagatgtg 180
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ctg gca aac agc ggg gcg atc cag gcg gct gac agc ctg act gca cgt	14784
Leu Ala Asn Ser Gly Ala Ile Gln Ala Ala Asp Ser Leu Thr Ala Arg	
915 920 925	
ctg acg ggt gag ctc gtc agc aca gcg ggc agc aaa gtc acc tcg aac	14832
Leu Thr Gly Glu Leu Val Ser Thr Ala Gly Ser Lys Val Thr Ser Asn	
930 935 940	
ggt gaa atg gcg ctc agt gca ctg aat tta agc aac agc gga caa tgg	14880
Gly Glu Met Ala Leu Ser Ala Leu Asn Leu Ser Asn Ser Gly Gln Trp	
945 950 955	
att gca aaa aat ctg acc ctg aag gcg aac tca ctg acc agt gcg ggt	14928
Ile Ala Lys Asn Leu Thr Leu Lys Ala Asn Ser Leu Thr Ser Ala Gly	
960 965 970 975	
gac atc acc ggt gtg gat act ctc acg ctc acg gtg aat cag acg ctg	14976
Asp Ile Thr Gly Val Asp Thr Leu Thr Leu Thr Val Asn Gln Thr Leu	
980 985 990	
aac aat cag gcg aac gga aaa ctg ctc agt gca ggt gtg ctg acg ctg	15024
Asn Asn Gln Ala Asn Gly Lys Leu Leu Ser Ala Gly Val Leu Thr Leu	
995 1000 1005	
aag gca gac agt gtc aca aac gac ggg caa tta cag gga aat gtc	15069
Lys Ala Asp Ser Val Thr Asn Asp Gly Gln Leu Gln Gly Asn Val	
1010 1015 1020	
acc acc atc acg gca gga caa ctc aca aac ggc ggc cat ctg cag	15114
Thr Thr Ile Thr Ala Gly Gln Leu Thr Asn Gly Gly His Leu Gln	
1025 1030 1035	
ggc gaa acg ctg acg ctg aca gcc tcc ggt ggc gtg aac aac cgt	15159
Gly Glu Thr Leu Thr Leu Thr Ala Ser Gly Gly Val Asn Asn Arg	
1040 1045 1050	
tcc ggt ggt gtt ctg atg agc cgg aat gca ctg aat gtc agt act	15204
Ser Gly Gly Val Leu Met Ser Arg Asn Ala Leu Asn Val Ser Thr	
1055 1060 1065	
gcg acc ctg agt aac cag agc acg ata cag ggt gga ggc ggg gtt	15249
Ala Thr Leu Ser Asn Gln Ser Thr Ile Gln Gly Gly Gly Gly Val	
1070 1075 1080	
tcc ctg aac gcc aca gac cgt ctg cag aac gac ggc aaa atc ctc	15294

0	Gly Phe Thr Gly Thr	Ala Gly Ser Leu Thr	Met Asn	
	1315	1320		
5	acc ctg ctg aac agt	gcg ctg att tat	gcg ggg aat	16014
	Thr Leu Leu Asn Ser	Ala Leu Ile Tyr	Ala Gly Asn	
	1330	1335		
0	ctg ttt aca gac cgt	ctg cat aac cag cat	ggg gat	16059
	Leu Phe Thr Asp Arg	Leu His Asn Gln His	Gly Asp	
	1345	1350		
5	ggc aac agt ctg tgg	gta cag aag gat	gct tcc ggc	16104
	Gly Asn Ser Leu Trp	Val Gln Lys Asp	Ala Ser Gly	
	1360	1365		
0	aca gag att atc aat	aat tcc ggg aat att	gag acg	16149
	Thr Glu Ile Ile Asn	Asn Ser Gly Asn Ile	Glu Thr	
	1375	1380		
5	gat att gtt gta aga	acc ggg cat ctt ctg	aac cag	16194
	Asp Ile Val Val Arg	Thr Gly His Leu Leu	Asn Gln	
	1390	1395		
0	ttt tct gcc aca aca	aca acc cgg act aac	ccc tca	16239
	Phe Ser Ala Thr Thr	Thr Thr Arg Thr Asn	Pro Ser	
	1405	1410		
5	gga atg gga aat gct	ctg gtt gat att ccc	ctt tcc	16284
	Gly Met Gly Asn Ala	Leu Val Asp Ile Pro	Leu Ser	
	1420	1425		
0	gac ggc agc tat ggc	tat ttc acc cgt gaa	gtt gaa	16329
	Asp Gly Ser Tyr Gly	Tyr Phe Thr Arg Glu	Val Glu	
	1435	1440		
5	ggt acg ccc tgc aac	ggg cac ggg gca tgc	aat atc	16374
	Gly Thr Pro Cys Asn	Gly His Gly Ala Cys	Asn Ile	
	1450	1455		
0	acg ctt tat tat tac	gcg ccg ttt gct gac	agt gcc	16419
	Thr Leu Tyr Tyr Tyr	Ala Pro Phe Ala Asp	Ser Ala	
	1465	1470		
5	ttt ctc agc agc cag	aac atc aca aca gta	acc ggt	16464
	Phe Leu Ser Ser Gln	Asn Ile Thr Thr Val	Thr Gly	
	1480	1485		
0	ccg gca ggc cgc att	gcg tca ggg cgt aat	ctt tct	16509
	Pro Ala Gly Arg Ile	Ala Ser Gly Arg Asn	Leu Ser	
	1495	1500		
5	gaa cga ctg gaa aac	cgg gcg tca ttt atc	ctg gcg	16554
	Glu Arg Leu Glu Asn	Arg Ala Ser Phe Ile	Leu Ala	
	1510	1515		
0	atc gca ctc tcg ggc	aga gag tta agc aat	cag agc	16599
	Ile Ala Leu Ser Gly	Arg Glu Leu Ser Asn	Gln Ser	
	1525	1530		
5	ggg aca gag aat gaa	tat ctg gta tac cgc	tac gac	16644

Ser Ser Tyr	Phe Leu Asp Arg Leu	Gly Leu Lys Pro Glu	Lys Asp	
1760	1765	1770		
tat cgt ttc	ctg ggg gat gcg gtc	ttt gat acc cgg tat	gtc agt	17364
Tyr Arg Phe	Leu Gly Asp Ala Val	Phe Asp Thr Arg Tyr	Val Ser	
1775	1780	1785		
aac gcg gtg	ctg agc cgg acg ggt	tca cgt tat ctc aac	gga ctg	17409
Asn Ala Val	Leu Ser Arg Thr Gly	Ser Arg Tyr Leu Asn	Gly Leu	
1790	1795	1800		
ggt tca gac	acg gaa cag atg cgg	tat ctg atg gat aac	gcg gcc	17454
Gly Ser Asp	Thr Glu Gln Met Arg	Tyr Leu Met Asp Asn	Ala Ala	
1805	1810	1815		
aga caa cag	aaa gga ctg gga tta	gag ttt ggt gtg gcg	ctg aca	17499
Arg Gln Gln	Lys Gly Leu Gly Leu	Glu Phe Gly Val Ala	Leu Thr	
1820	1825	1830		
gct gaa cag	att gct cag ctt gac	ggc agc ata ctg tgg	tgg gag	17544
Ala Glu Gln	Ile Ala Gln Leu Asp	Gly Ser Ile Leu Trp	Trp Glu	
1835	1840	1845		
tca gtc acc	atc aac gga caa aca	gtc atg gtc ccg aaa	ctg tat	17589
Ser Val Thr	Ile Asn Gly Gln Thr	Val Met Val Pro Lys	Leu Tyr	
1850	1855	1860		
ctg tcg ccg	gaa gat atc acc ctg	cat aac ggc agc gtt	atc agc	17634
Leu Ser Pro	Glu Asp Ile Thr Leu	His Asn Gly Ser Val	Ile Ser	
1865	1870	1875		
ggg aac aac	gtg caa ctt gcg ggc	ggc aat atc acc aac	agc ggc	17679
Gly Asn Asn	Val Gln Leu Ala Gly	Gly Asn Ile Thr Asn	Ser Gly	
1880	1885	1890		
ggc agc atc	aac gca cag aac gac	ctc tcg ctc gac agt	tcc ggc	17724
Gly Ser Ile	Asn Ala Gln Asn Asp	Leu Ser Leu Asp Ser	Ser Gly	
1895	1900	1905		
tat atc gac	aac ctg aat gcg ggg	ctg ata agc gcg ggc	ggt agc	17769
Tyr Ile Asp	Asn Leu Asn Ala Gly	Leu Ile Ser Ala Gly	Gly Ser	
1910	1915	1920		
ctg gac ctg	agc gcc atc ggg gat	atc agc aat atc agc	tca gtc	17814
Leu Asp Leu	Ser Ala Ile Gly Asp	Ile Ser Asn Ile Ser	Ser Val	
1925	1930	1935		
atc agc ggt	aaa acc gta caa ctg	gaa agc gtg agt ggc	aac atc	17859
Ile Ser Gly	Lys Thr Val Gln Leu	Glu Ser Val Ser Gly	Asn Ile	
1940	1945	1950		
agc aat atc	acc cgg cgt cag caa	tgg aat gcg ggc agt	gac agc	17904
Ser Asn Ile	Thr Arg Arg Gln Gln	Trp Asn Ala Gly Ser	Asp Ser	
1955	1960	1965		
caa tat ggt	ggt gtg cat ctc agc	ggt acg gac acc ggt	ccg gtt	17949
Gln Tyr Gly	Gly Val His Leu Ser	Gly Thr Asp Thr Gly	Pro Val	
1970	1975	1980		
gcg acc att	aaa ggc act gat tca	ctt tcg ctg gat gca	ggg aaa	17994

Ala	Thr	Ile	Lys	Gly	Thr	Asp	Ser	Leu	Ser	Leu	Asp	Ala	Gly	Lys	
		1985					1990					1995			
aac	att	gat	att	acc	ggg	gca	acg	gtc	tcg	tcc	ggt	gga	gac	ctt	18039
Asn	Ile	Asp	Ile	Thr	Gly	Ala	Thr	Val	Ser	Ser	Gly	Gly	Asp	Leu	
		2000					2005					2010			
gga	atg	tct	gcg	ggt	aat	gat	atc	aac	att	gcc	gca	aac	ctg	ata	18084
Gly	Met	Ser	Ala	Gly	Asn	Asp	Ile	Asn	Ile	Ala	Ala	Asn	Leu	Ile	
		2015					2020					2025			
agt	ggg	agc	aaa	agt	cag	tcc	ggt	ttc	tgg	cac	act	gat	gac	aac	18129
Ser	Gly	Ser	Lys	Ser	Gln	Ser	Gly	Phe	Trp	His	Thr	Asp	Asp	Asn	
		2030					2035					2040			
agt	tca	tca	tcc	acc	acc	tca	cag	ggc	agc	agc	atc	agc	gcc	ggc	18174
Ser	Ser	Ser	Ser	Thr	Thr	Ser	Gln	Gly	Ser	Ser	Ile	Ser	Ala	Gly	
		2045					2050					2055			
ggt	aac	ctg	gcg	atg	gct	gca	ggc	cat	aat	ctg	gat	gtc	acg	gca	18219
Gly	Asn	Leu	Ala	Met	Ala	Ala	Gly	His	Asn	Leu	Asp	Val	Thr	Ala	
		2060					2065					2070			
tcc	tct	gtt	tct	gcc	ggg	cac	agc	gcc	ctg	ctt	tct	gca	ggt	aac	18264
Ser	Ser	Val	Ser	Ala	Gly	His	Ser	Ala	Leu	Leu	Ser	Ala	Gly	Asn	
		2075					2080					2085			
gac	ctg	agt	ctg	aat	gca	gtc	agg	gaa	agc	aaa	aac	agt	cgc	aac	18309
Asp	Leu	Ser	Leu	Asn	Ala	Val	Arg	Glu	Ser	Lys	Asn	Ser	Arg	Asn	
		2090					2095					2100			
ggc	agg	tca	gaa	agt	cat	gaa	agc	cac	gca	gct	gtg	tcc	acg	gtg	18354
Gly	Arg	Ser	Glu	Ser	His	Glu	Ser	His	Ala	Ala	Val	Ser	Thr	Val	
		2105					2110					2115			
aca	gcg	ggc	gat	aac	ttc	ctc	ctt	gtt	gcc	ggt	cgt	gat	att	gcc	18399
Thr	Ala	Gly	Asp	Asn	Phe	Leu	Leu	Val	Ala	Gly	Arg	Asp	Ile	Ala	
		2120					2125					2130			
agt	cag	gct	gcc	ggt	atg	gct	gcg	gaa	aat	aac	gtg	gtc	atc	cgg	18444
Ser	Gln	Ala	Ala	Gly	Met	Ala	Ala	Glu	Asn	Asn	Val	Val	Ile	Arg	
		2135					2140					2145			
ggc	gga	cgt	gat	gtg	aac	ctg	gtg	gca	gag	tct	gcc	ggc	gca	ggc	18489
Gly	Gly	Arg	Asp	Val	Asn	Leu	Val	Ala	Glu	Ser	Ala	Gly	Ala	Gly	
		2150					2155					2160			
gac	agc	tat	acg	tcg	aag	aaa	aag	aaa	gag	att	aac	gag	aca	gtc	18534
Asp	Ser	Tyr	Thr	Ser	Lys	Lys	Lys	Lys	Glu	Ile	Asn	Glu	Thr	Val	
		2165					2170					2175			
cgt	cag	cag	gga	acg	gaa	atc	gcc	agc	ggt	ggt	gac	acc	acc	gtc	18579
Arg	Gln	Gln	Gly	Thr	Glu	Ile	Ala	Ser	Gly	Gly	Asp	Thr	Thr	Val	
		2180					2185					2190			
aac	gca	gga	cgg	gat											

Thr Gly Asn	Ile Ser Val Asn	Ala	Gly Arg Asp Val	Ala	Leu Thr	
2210		2215		2220		
acg gcg aca	gaa agt gac tat	cac	tat ctg gaa acg	aag	aaa aaa	18714
Thr Ala Thr	Glu Ser Asp Tyr	His	Tyr Leu Glu Thr	Lys	Lys Lys	
2225		2230		2235		
agc gga ggt	ttt ctc agt aag	aaa	acc acc cgc acc	atc	agt gag	18759
Ser Gly Gly	Phe Leu Ser Lys	Lys	Thr Thr Arg Thr	Ile	Ser Glu	
2240		2245		2250		
gac agt gcc	acc cgt gaa gca	ggc	tcc ctg ctg tcg	ggg	aac cgc	18804
Asp Ser Ala	Thr Arg Glu Ala	Gly	Ser Leu Leu Ser	Gly	Asn Arg	
2255		2260		2265		
gtg acc gtt	aac gcc ggt gat	aac	ctg acg gta gag	ggt	tcg gat	18849
Val Thr Val	Asn Ala Gly Asp	Asn	Leu Thr Val Glu	Gly	Ser Asp	
2270		2275		2280		
gtg gtg gct	gac cgg gat gtg	tca	ctg gcg gcg ggt	aac	cat gtt	18894
Val Val Ala	Asp Arg Asp Val	Ser	Leu Ala Ala Gly	Asn	His Val	
2285		2290		2295		
gat gtt ctt	gct gcc acc agt	aca	gat acg tcc tgg	cgc	ttt aag	18939
Asp Val Leu	Ala Ala Thr Ser	Thr	Asp Thr Ser Trp	Arg	Phe Lys	
2300		2305		2310		
gaa acg aag	aaa tcc ggt ctg	atg	ggt acc gcc ggt	att	ggt ttc	18984
Glu Thr Lys	Lys Ser Gly Leu	Met	Gly Thr Gly Gly	Ile	Gly Phe	
2315		2320		2325		
acc att ggc	agc agt aag aca	acg	cac gac cgg cgc	gag	gcc ggg	19029
Thr Ile Gly	Ser Ser Lys Thr	Thr	His Asp Arg Arg	Glu	Ala Gly	
2330		2335		2340		
aca acg cag	agt cag agt gcc	agc	acc atc gcc tcc	act	gcc ggt	19074
Thr Thr Gln	Ser Gln Ser Ala	Ser	Thr Ile Gly Ser	Thr	Ala Gly	
2345		2350		2355		
aat gtc agt	att acc gcg gcc	aaa	cag gct cat atc	agc	ggt tcg	19119
Asn Val Ser	Ile Thr Ala Gly	Lys	Gln Ala His Ile	Ser	Gly Ser	
2360		2365		2370		
gat gtg att	gcg aac cgg gat	atc	agc att acc ggt	gac	agt gtg	19164
Asp Val Ile	Ala Asn Arg Asp	Ile	Ser Ile Thr Gly	Asp	Ser Val	
2375		2380		2385		
gtg gtt gac	ccg ggg cat gac	cgt	cgt act gtg gac	gaa	aaa ttt	19209
Val Val Asp	Pro Gly His Asp	Arg	Arg Thr Val Asp	Glu	Lys Phe	
2390		2395		2400		
gag cag aag	aaa agc ggg ctg	acg	gtt gcc ctt tcc	ggc	acg gtg	19254
Glu Gln Lys	Lys Ser Gly Leu	Thr	Val Ala Leu Ser	Gly	Thr Val	
2405		2410		2415		
ggc agt gcc	atc aat aat gcg	gtt	acc agt gca cag	gag	acg aag	19299
Gly Ser Ala	Ile Asn Asn Ala	Val	Thr Ser Ala Gln	Glu	Thr Lys	
2420		2425		2430		
gag agc agt	gac agc cgt ctg	aaa	gcc ctg cag gcc	aca	aag aca	19344

Glu Ser Ser	Asp Ser Arg Leu Lys	Ala Leu Gln Ala Thr	Lys Thr	
2435	2440	2445		
gcg ctg tct	ggg gtg cag gcc gga	cag gct gcg aca atg	gcc tcc	19389
Ala Leu Ser	Gly Val Gln Ala Gly	Gln Ala Ala Thr Met	Ala Ser	
2450	2455	2460		
gca acc ggt	gac ccg aat gcg atg	gga gtc agc ctg tcg	ctc acc	19434
Ala Thr Gly	Asp Pro Asn Ala Met	Gly Val Ser Leu Ser	Leu Thr	
2465	2470	2475		
acc cag aaa	tcg aaa tca caa caa	cat tct gaa agt gac	aca gta	19479
Thr Gln Lys	Ser Lys Ser Gln Gln	His Ser Glu Ser Asp	Thr Val	
2480	2485	2490		
tcc ggc agt	acg ctg aat gcc ggg	aat aat ctg tct gtt	gtc gca	19524
Ser Gly Ser	Thr Leu Asn Ala Gly	Asn Asn Leu Ser Val	Val Ala	
2495	2500	2505		
acc ggt aaa	aac agg ggc gat aac	cgc gga gat att gtg	att gcc	19569
Thr Gly Lys	Asn Arg Gly Asp Asn	Arg Gly Asp Ile Val	Ile Ala	
2510	2515	2520		
gga agc cag	ctt aag gcc ggt ggt	aac aca agc ctg gat	gcc gcg	19614
Gly Ser Gln	Leu Lys Ala Gly Gly	Asn Thr Ser Leu Asp	Ala Ala	
2525	2530	2535		
aat gat att	ctg ttg agt ggc gcc	gca aac aca caa aaa	aca acg	19659
Asn Asp Ile	Leu Leu Ser Gly Ala	Ala Asn Thr Gln Lys	Thr Thr	
2540	2545	2550		
ggc agg aac	agc agc agt ggc ggt	ggc gtg ggt gtc agt	atc ggt	19704
Gly Arg Asn	Ser Ser Ser Gly Gly	Gly Val Gly Val Ser	Ile Gly	
2555	2560	2565		
gcc ggt ggt	aac ggt gcc ggt atc	agc gtc ttt gcc ggc	gtt aat	19749
Ala Gly Gly	Asn Gly Ala Gly Ile	Ser Val Phe Ala Gly	Val Asn	
2570	2575	2580		
gcg gca aaa	ggc agc gag aaa ggt	aac ggt act gag tgg	act gaa	19794
Ala Ala Lys	Gly Ser Glu Lys Gly	Asn Gly Thr Glu Trp	Thr Glu	
2585	2590	2595		
acc aca aca	gac agc ggt aaa acc	gtc acc atc aac agt	ggg cgg	19839
Thr Thr Thr	Asp Ser Gly Lys Thr	Val Thr Ile Asn Ser	Gly Arg	
2600	2605	2610		
gat acg gta	ctg aac ggt gct cag	gtc aac ggc aac agg	att atc	19884
Asp Thr Val	Leu Asn Gly Ala Gln	Val Asn Gly Asn Arg	Ile Ile	
2615	2620	2625		
gcc gat gtg	ggc cac gac ctg ctg	ata agc agc cag cag	gac acc	19929
Ala Asp Val	Gly His Asp Leu Leu	Ile Ser Ser Gln Gln	Asp Thr	
2630	2635	2640		
agt aag tac	gac agt aaa cag acc	agc gtg gct gcc ggc	ggc agt	19974
Ser Lys Tyr	Asp Ser Lys Gln Thr	Ser Val Ala Ala Gly	Gly Ser	
2645	2650	2655		
ttt acc ttt	ggc tcc atg acc ggc	tca ggt tac atc gct	gcc tcc	20019

20064 20109 20154 20199 20244 20289 20334 20379 20424 20469 20518 20578 20638 20698 20758 20818 20878 20938

Phe Thr Phe Gly Ser Met Thr Gly Ser Gly Tyr Ile Ala Ala Ser	2660	2665	2670	
cgg gat aag atg aag agc cgc ttt gac tcc gtt gct gaa caa acc	2675	2680	2685	20064
Arg Asp Lys Met Lys Ser Arg Phe Asp Ser Val Ala Glu Gln Thr				
gga atg ttt gcc ggt gat ggt ggc ttc gac att aca gtg ggc aga	2690	2695	2700	20109
Gly Met Phe Ala Gly Asp Gly Gly Phe Asp Ile Thr Val Gly Arg				
cat acc caa ctg gat ggt gcg gtg att gcc tcc act gcc aca ccg	2705	2710	2715	20154
His Thr Gln Leu Asp Gly Ala Val Ile Ala Ser Thr Ala Thr Pro				
gat aaa aac cac ctg gat acc gga acg ctg ggg ttc agt gac ctt	2720	2725	2730	20199
Asp Lys Asn His Leu Asp Thr Gly Thr Leu Gly Phe Ser Asp Leu				
cac aac gaa gcg gat tat aaa gtc agt cac agt gga atc agt ctg	2735	2740	2745	20244
His Asn Glu Ala Asp Tyr Lys Val Ser His Ser Gly Ile Ser Leu				
agc ggt ggt gcc agc ttc ggg gat aaa ttt cag ggt aac atg ccg	2750	2755	2760	20289
Ser Gly Gly Gly Ser Phe Gly Asp Lys Phe Gln Gly Asn Met Pro				
ggt gcc atg ata tcc gcc gga ggt cac agc gga cat gcg gaa gga	2765	2770	2775	20334
Gly Gly Met Ile Ser Ala Gly Gly His Ser Gly His Ala Glu Gly				
acg act cag gcc gca gtg gca gaa ggc act atc acc atc cgg gac	2780	2785	2790	20379
Thr Thr Gln Ala Ala Val Ala Glu Gly Thr Ile Thr Ile Arg Asp				
agg gac aat cag aag cag aat ctg gcg aac ctg agc cgt gac cct	2795	2800	2805	20424
Arg Asp Asn Gln Lys Gln Asn Leu Ala Asn Leu Ser Arg Asp Pro				
gcg cac gct aat gac agt atc agc ccg ata ttt gac aag gag aaa	2810	2815	2820	20469
Ala His Ala Asn Asp Ser Ile Ser Pro Ile Phe Asp Lys Glu Lys				
gag cag agg cgt ctg cag aca gtg ggg ctt atc aag tga cataggcagt	2825	2830		20518
Glu Gln Arg Arg Leu Gln Thr Val Gly Leu Ile Lys				
caggtggcgg atattgcgcg tacacaggga gaactgaatg cgttgaaggc cgcgaaggaa				20578
gcaaccggcg aaacacttcc tgctaattgca acagagaaac aacgtcagga atatcttgcg				20638
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aaagacccgg cagtaaagc cattgctcac gccattctgg gcggcgagcagg ggcggcaatg				20878
cagggtaata atgtcgctgc cggtgcagca ggcgagagct ggcagccaga				20938

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Arg Lys Lys Glu	Glu Asp Thr Glu Val	Arg Ile Glu Gly Phe Trp	
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Glu Glu Cys Gln	Pro Gly Glu Thr Gln	Cys Thr Ala Val Phe Asn	
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Ile Val Gly Glu	Asp Gly Gln Val Thr	Glu Ala Val Leu Thr Gln	
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Asp Gly Pro Val	Leu Asp Asp Ile Thr	Ala Gly Gln Ser Gly Thr	
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Ala Phe Gly Gly	Gly Leu Ala Ala Met	Ala Leu Ala Ala Gly Gly	
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Gly Gly Ser Lys	His Arg His Glu Asn	Asp Asp Ser Asp Thr Thr	
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Ser Val Glu Leu	Pro Gly Asp Ala Asn	Lys Gly Asp Thr Val Asp	
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Glu Lys Gly Asp	Asn Gly Trp Thr Ser	Ser Asp Pro Thr Leu Ile	
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Pro Asp Ser Thr	Gly Asp Lys Ala Thr	Ile Pro Ala Asp Asn Val	
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Ala Asp Ala Pro Val Leu Ser Ile Pro Glu Val Thr Asp Gly Tyr	3105	3110	3115	
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Ala Asn Ala Asp Glu Leu Lys Asp Gly Leu Gln Ala Glu Val Thr				
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Leu Pro Ala Gly Thr Ala Glu Gly Ala Val Ile Thr Leu Thr Val				
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Thr Arg Pro Asp Lys Thr Thr Glu Asn Val Thr His Thr Val Thr				
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Lys Asp Glu Val Ala Ala Gly Lys Val Ser Met Asp Ile Pro Lys				
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Asp Ala Val Ile Asp Gly Gln Asn Ser Val Ser Val Thr Leu Thr				
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Gln Gly Ser Asn Pro Ala Lys Pro Gly Asn Val Val Asp Phe Ala				
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Pro Lys Gly Ser Ala Ala Gly Asp Thr Leu Thr Leu Thr Val Thr				
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Lys Pro Asp Gly Thr Thr Asp Thr Val Glu His Thr Leu Thr Ala				
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His Thr Leu Thr Ala Asp Glu Val Ala Ala Gly Lys Ala Asp Val				
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Gln Pro Ala Asp Phe Ala Val Asp Thr Val Ala Pro Ser Ala Pro				
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Glu Lys Gly Gly Lys His Thr Val Thr Leu Glu Lys Gly Asp Asn				
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tgcaattaaa tgcttatccg gtattgatca cagagatgga aatatcacia tgattaataa 47719
cataattact gctaataata tcgtaatttt gaaagtggta atcctgttca cggcactata 47779
attagagtta tgtcttgtat ccgttcagta taatttcacg aatgctttat taaccggatg 47839
cgtgaatgtc attcttcaga tgacaaagac gtcacgcgca ttgatggaaa agcaacttcca 47899
cactcctatg ataaaagccg tcgcaggaga gcgggctttc gtagtcttac ccgactctc 47959
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<210> 252
<211> 2834
<212> PRT
<213> Escherichia coli

<220>
<221> misc_feature
<222> (493)..(493)
<223> The 'Xaa' at location 493 stands for Asn, Asp, His, or Tyr.

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<222> (1158)..(1158)
<223> The 'Xaa' at location 1158 stands for Asp, or Tyr.

<220>
<221> misc_feature
<222> (1159)..(1159)
<223> The 'Xaa' at location 1159 stands for Leu.

<220>
<221> misc_feature
<222> (1168)..(1168)
<223> The 'Xaa' at location 1168 stands for Ser, or Asn.

<220>
<221> misc_feature
<222> (1270)..(1270)
<223> The 'Xaa' at location 1270 stands for Thr, or Pro.

<220>
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<222> (13480)..(13480)
<223> Unsure

<220>
<221> misc_feature
<222> (31038)..(31038)

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<223> Unsure

<220>

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<222> (31042)..(31042)

<223> Unsure

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<222> (31799)..(31799)

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<220>

<221> misc_feature

<222> (44922)..(44922)

<223> Unsure

<400> 252

Met His Gln Pro Pro Val Arg Phe Thr Tyr Arg Leu Leu Ser Tyr Leu
1 5 10 15

Val Ser Ala Ile Ile Ala Gly Gln Pro Leu Leu Pro Ala Val Gly Ala
20 25 30

Val Ile Thr Pro Gln Asn Gly Ala Gly Met Asp Lys Ala Ala Asn Gly
35 40 45

Val Pro Val Val Asn Ile Ala Thr Pro Asn Gly Ala Gly Ile Ser His
50 55 60

Asn Arg Phe Thr Asp Tyr Asn Val Gly Lys Glu Gly Leu Ile Leu Asn
65 70 75 80

Asn Ala Thr Gly Lys Leu Asn Pro Thr Gln Leu Gly Gly Leu Ile Gln
85 90 95

Asn Asn Pro Asn Leu Lys Ala Gly Gly Glu Ala Lys Gly Ile Ile Asn
100 105 110

Glu Val Thr Gly Gly Lys Arg Ser Leu Leu Gln Gly Tyr Thr Glu Val
115 120 125

Ala Gly Lys Ala Ala Asn Val Met Val Ala Asn Pro Tyr Gly Ile Thr
130 135 140

Cys Asp Gly Cys Gly Phe Ile Asn Thr Pro His Ala Thr Leu Thr Thr
145 150 155 160

Gly Lys Pro Val Met Asn Ala Asp Gly Ser Leu Gln Ala Leu Glu Val
165 170 175

Thr Glu Gly Ser Ile Thr Ile Asn Gly Ala Gly Leu Asp Gly Thr Arg
180 185 190

Ser Asp Ala Val Ser Ile Ile Ala Arg Ala Thr Glu Val Asn Ala Ala
195 200 205

Leu His Ala Lys Asp Leu Thr Val Thr Ala Gly Ala Asn Arg Val Thr
210 215 220

Ala Asp Gly Arg Val Arg Ala Leu Lys Gly Glu Gly Asp Val Pro Lys
225 230 235 240

Val Ala Val Asp Thr Gly Ala Leu Gly Gly Met Tyr Ala Arg Arg Ile
245 250 255

His Leu Thr Ser Thr Glu Ser Gly Val Gly Val Asn Leu Gly Asn Leu
260 265 270

Tyr Ala Arg Asp Gly Asp Ile Thr Leu Asp Ala Ser Gly Arg Leu Thr
275 280 285

Val Asn Asn Ser Leu Ala Thr Gly Ala Val Thr Ala Lys Gly Gln Gly
290 295 300

Val Thr Leu Thr Gly Asp His Lys Ala Gly Gly Asn Leu Ser Val Ser
305 310 315 320

Ser Arg Arg Asp Ile Val Leu Ser Asn Gly Thr Leu Asn Ser Asp Lys
325 330 335

Asp Leu Ser Leu Thr Ala Gly Gly Arg Ile Thr Gln Gln Asn Glu Lys
340 345 350

Leu Thr Ala Gly Arg Asp Val Thr Leu Ala Ala Lys Asn Ile Thr Gln
355 360 365

Asp Thr Ala Ser Gln Ile Asn Ala Ala Arg Asp Ile Val Thr Val Ala
370 375 380

Ser Asp Thr Leu Thr Thr Gln Gly Gln Ile Thr Ala Gly Gln Asn Leu
385 390 395 400

Thr Ala Ser Ala Thr Thr Leu Thr Gln Asp Gly Ile Leu Leu Ala Lys
405 410 415

Ser His Ala Gly Leu Asn Ala Gly Thr Leu Asn Asn Ser Gly Ala Val
420 425 430

Gln Gly Ala Thr Leu Thr Leu Gly Ser Thr Thr Leu Ser Asn Ser Gly
435 440 445

Ser Leu Leu Ser Gly Gly Pro Leu Thr Met Asn Thr Arg Asp Phe Thr
450 455 460

Gln Ser Gly Arg Thr Gly Ala Lys Gly Lys Val Asp Ile Met Ala Ser
465 470 475 480

Gly Lys Leu Thr Ser Thr Gly Leu Leu Val Ser Asp Xaa Ala Leu Val
485 490 495

Leu Lys Ala Gln Asp Val Thr Gln Asn Gly Val Leu Ser Gly Gly Lys
500 505 510

Gly Leu Thr Val Ser Ala Gln Thr Leu Ser Ser Gly Lys Lys Ser Val
515 520 525

Thr His Ser Asp Ala Ala Met Thr Leu Asn Val Thr Thr Val Ala Leu
530 535 540

Asp Gly Glu Thr Ser Ala Gly Asp Thr Leu Arg Val Gln Ala Asp Lys
545 550 555 560

Leu Ser Thr Ala Ala Gly Ala Gln Leu Gln Ser Gly Lys Asn Leu Ser
565 570 575

Ile Asn Ala Arg Asp Ala Arg Leu Ala Gly Thr Gln Ala Ala Gln Gln
580 585 590

Thr Met Val Val Asn Ala Ser Glu Lys Leu Thr His Ser Gly Lys Ser
595 600 605

Ser Ala Pro Ser Leu Ser Leu Ser Ala Pro Glu Leu Thr Ser Ser Gly
610 615 620

Val Leu Val Gly Ser Ala Leu Asn Thr Gln Ser Gln Thr Leu Thr Asn
625 630 635 640

Ser Gly Leu Leu Gln Gly Glu Ala Ser Leu Thr Val Asn Thr Gln Arg
645 650 655

Leu Asp Asn Gln Gln Asn Gly Thr Leu Tyr Ser Ala Ala Asp Leu Thr
660 665 670

Leu Asp Ile Pro Asp Ile Arg Asn Ser Gly Leu Ile Thr Gly Asp Asn
675 680 685

Gly Leu Met Leu Asn Ala Val Ser Leu Ser Asn Pro Gly Lys Ile Ile
690 695 700

Ala Asp Thr Leu Ser Val Arg Ala Thr Thr Leu Asp Gly Asp Gly Leu
705 710 715 720

Leu Gln Gly Ala Gly Ala Leu Ala Leu Ala Gly Asp Thr Leu Ser Gln
725 730 735

Gly Ser His Gly Arg Trp Leu Thr Ala Asp Asp Leu Ser Leu Arg Gly
740 745 750

Lys Thr Leu Asn Thr Ala Gly Thr Thr Gln Gly Gln Asn Ile Thr Val
755 760 765

Gln Ala Asp Arg Trp Ala Asn Ser Gly Ser Val Leu Ala Thr Gly Asn
770 775 780

Leu Thr Ala Ser Ala Thr Gly Gln Leu Thr Ser Thr Gly Asp Ile Met
785 790 795 800

Ser Gln Gly Asp Thr Thr Leu Lys Ala Ala Thr Thr Asp Asn Arg Gly
805 810 815

Ser Leu Leu Ser Ala Gly Thr Leu Ser Leu Asp Gly Asn Ser Leu Asp
820 825 830

Asn Arg Gly Thr Val Gln Gly Asn His Val Thr Ile Arg Gln Asn Ser
835 840 845

Val Thr Asn Ser Gly Thr Leu Thr Gly Ile Ala Ala Leu Thr Leu Ala
850 855 860

Ala Arg Met Ala Ser Pro Gln Pro Ala Leu Met Asn Asn Gly Gly Ser
865 870 875 880

Leu Leu Thr Ser Gly Asp Leu Thr Ile Thr Ala Gly Ser Ile Thr Ser
885 890 895

Ser Gly His Trp Gln Gly Lys Arg Val Leu Ile Thr Ala Asp Ser Leu
900 905 910

Ala Asn Ser Gly Ala Ile Gln Ala Ala Asp Ser Leu Thr Ala Arg Leu
915 920 925

Thr Gly Glu Leu Val Ser Thr Ala Gly Ser Lys Val Thr Ser Asn Gly
930 935 940

Glu Met Ala Leu Ser Ala Leu Asn Leu Ser Asn Ser Gly Gln Trp Ile
945 950 955 960

Ala Lys Asn Leu Thr Leu Lys Ala Asn Ser Leu Thr Ser Ala Gly Asp
965 970 975

Ile Thr Gly Val Asp Thr Leu Thr Leu Thr Val Asn Gln Thr Leu Asn
980 985 990

Asn Gln Ala Asn Gly Lys Leu Leu Ser Ala Gly Val Leu Thr Leu Lys
995 1000 1005

Ala Asp Ser Val Thr Asn Asp Gly Gln Leu Gln Gly Asn Val Thr
1010 1015 1020

Thr Ile Thr Ala Gly Gln Leu Thr Asn Gly Gly His Leu Gln Gly
1025 1030 1035

Glu Thr Leu Thr Leu Thr Ala Ser Gly Gly Val Asn Asn Arg Ser
1040 1045 1050

Gly Gly Val Leu Met Ser Arg Asn Ala Leu Asn Val Ser Thr Ala
1055 1060 1065

Thr Leu Ser Asn Gln Ser Thr Ile Gln Gly Gly Gly Gly Val Ser
1070 1075 1080

Leu Asn Ala Thr Asp Arg Leu Gln Asn Asp Gly Lys Ile Leu Ser
1085 1090 1095

Gly Ser Asn Leu Thr Leu Thr Ala Gln Val Leu Ala Asn Thr Gly
1100 1105 1110

Ser Gly Leu Val Gln Ala Ala Thr Leu Leu Leu Asp Val Val Asn
1115 1120 1125

Thr Val Asn Gly Gly Arg Val Leu Ala Thr Gly Ser Ala Asp Val
1130 1135 1140

Lys Gly Thr Thr Leu Asn Asn Thr Gly Thr Leu Gln Gly Ala Xaa
1145 1150 1155

Xaa Leu Val Asn Tyr His Thr Phe Ser Xaa Ser Gly Thr Leu Leu
1160 1165 1170

Gly Thr Ser Gly Leu Gly Val Lys Gly Ser Ser Leu Leu Gln Asn
1175 1180 1185

Gly Thr Gly Arg Leu Tyr Ser Ala Gly Asn Leu Leu Leu Asp Ala
1190 1195 1200

Gln Asp Phe Ser Gly Gln Gly Gln Val Val Ala Thr Gly Asp Val
1205 1210 1215

Thr Leu Lys Leu Ile Ala Ala Leu Thr Asn His Gly Thr Leu Ala
1220 1225 1230

Ala Gly Lys Thr Leu Ser Val Thr Ser Gln Asn Ala Ile Thr Asn
1235 1240 1245

Gly Gly Val Met Gln Gly Asp Ala Met Val Leu Gly Ala Gly Glu
1250 1255 1260

Ala Phe Thr Asn Asn Gly Xaa Leu Thr Ala Gly Lys Gly Asn Ser
1265 1270 1275

Val Phe Ser Ala Gln Arg Leu Phe Leu Asn Ala Pro Gly Ser Leu
1280 1285 1290

Gln Gly Gly Gly Asp Val Ser Leu Asn Ser Arg Ser Asp Ile Thr
1295 1300 1305

Ile Ser Gly Phe Thr Gly Thr Ala Gly Ser Leu Thr Met Asn Val
1310 1315 1320

Ala Gly Thr Leu Leu Asn Ser Ala Leu Ile Tyr Ala Gly Asn Asn
1325 1330 1335

Leu Lys Leu Phe Thr Asp Arg Leu His Asn Gln His Gly Asp Ile
1340 1345 1350

Leu Ala Gly Asn Ser Leu Trp Val Gln Lys Asp Ala Ser Gly Gly
1355 1360 1365

Ala Asn Thr Glu Ile Ile Asn Asn Ser Gly Asn Ile Glu Thr His
1370 1375 1380

Gln Gly Asp Ile Val Val Arg Thr Gly His Leu Leu Asn Gln Arg
1385 1390 1395

Glu Gly Phe Ser Ala Thr Thr Thr Thr Arg Thr Asn Pro Ser Ser
1400 1405 1410

Ile Gln Gly Met Gly Asn Ala Leu Val Asp Ile Pro Leu Ser Leu
1415 1420 1425

Leu Pro Asp Gly Ser Tyr Gly Tyr Phe Thr Arg Glu Val Glu Asn
1430 1435 1440

Gln His Gly Thr Pro Cys Asn Gly His Gly Ala Cys Asn Ile Thr
1445 1450 1455

Met Asp Thr Leu Tyr Tyr Tyr Ala Pro Phe Ala Asp Ser Ala Thr
1460 1465 1470

Gln Arg Phe Leu Ser Ser Gln Asn Ile Thr Thr Val Thr Gly Ala
1475 1480 1485

Asp Asn Pro Ala Gly Arg Ile Ala Ser Gly Arg Asn Leu Ser Ala
1490 1495 1500

Glu Ala Glu Arg Leu Glu Asn Arg Ala Ser Phe Ile Leu Ala Asn
1505 1510 1515

Gly Asp Ile Ala Leu Ser Gly Arg Glu Leu Ser Asn Gln Ser Trp
1520 1525 1530

Gln Thr Gly Thr Glu Asn Glu Tyr Leu Val Tyr Arg Tyr Asp Pro
1535 1540 1545

Lys	Thr	Phe	Tyr	Gly	Ser	Tyr	Ala	Thr	Gly	Ser	Leu	Asp	Lys	Leu
1550						1555					1560			
Pro	Leu	Leu	Ser	Pro	Glu	Phe	Glu	Asn	Asn	Thr	Ile	Arg	Phe	Ser
1565						1570					1575			
Leu	Asp	Gly	Arg	Glu	Lys	Asp	Tyr	Thr	Pro	Gly	Lys	Thr	Tyr	Tyr
1580						1585					1590			
Ser	Val	Ile	Gln	Ala	Gly	Gly	Asp	Val	Lys	Thr	Arg	Phe	Thr	Ser
1595						1600					1605			
Ser	Ile	Asn	Asn	Gly	Thr	Thr	Thr	Ala	His	Ala	Gly	Ser	Val	Ser
1610						1615					1620			
Pro	Val	Val	Ser	Ala	Pro	Val	Leu	Asn	Thr	Leu	Ser	Gln	Gln	Thr
1625						1630					1635			
Gly	Gly	Asp	Ser	Leu	Thr	Gln	Thr	Ala	Leu	Gln	Gln	Tyr	Glu	Pro
1640						1645					1650			
Val	Val	Val	Gly	Ser	Pro	Gln	Trp	His	Asp	Glu	Leu	Ala	Gly	Ala
1655						1660					1665			
Leu	Lys	Asn	Ile	Ala	Gly	Gly	Ser	Pro	Leu	Thr	Gly	Gln	Thr	Gly
1670						1675					1680			
Ile	Ser	Asp	Asp	Trp	Pro	Leu	Pro	Ser	Gly	Asn	Asn	Gly	Tyr	Leu
1685						1690					1695			
Val	Pro	Ser	Thr	Asp	Pro	Asp	Ser	Pro	Tyr	Leu	Ile	Thr	Val	Asn
1700						1705					1710			
Pro	Lys	Leu	Asp	Gly	Leu	Gly	Gln	Val	Asp	Ser	His	Leu	Phe	Ala
1715						1720					1725			
Gly	Leu	Tyr	Glu	Leu	Leu	Gly	Ala	Lys	Pro	Gly	Gln	Ala	Pro	Arg
1730						1735					1740			
Glu	Thr	Ala	Pro	Ser	Tyr	Thr	Asp	Glu	Lys	Gln	Phe	Leu	Gly	Ser
1745						1750					1755			
Ser	Tyr	Phe	Leu	Asp	Arg	Leu	Gly	Leu	Lys	Pro	Glu	Lys	Asp	Tyr
1760						1765					1770			

1775 1780 1785 1790 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995

Arg	Phe	Leu	Gly	Asp	Ala	Val	Phe	Asp	Thr	Arg	Tyr	Val	Ser	Asn
1775						1780					1785			
Ala	Val	Leu	Ser	Arg	Thr	Gly	Ser	Arg	Tyr	Leu	Asn	Gly	Leu	Gly
1790						1795					1800			
Ser	Asp	Thr	Glu	Gln	Met	Arg	Tyr	Leu	Met	Asp	Asn	Ala	Ala	Arg
1805						1810					1815			
Gln	Gln	Lys	Gly	Leu	Gly	Leu	Glu	Phe	Gly	Val	Ala	Leu	Thr	Ala
1820						1825					1830			
Glu	Gln	Ile	Ala	Gln	Leu	Asp	Gly	Ser	Ile	Leu	Trp	Trp	Glu	Ser
1835						1840					1845			
Val	Thr	Ile	Asn	Gly	Gln	Thr	Val	Met	Val	Pro	Lys	Leu	Tyr	Leu
1850						1855					1860			
Ser	Pro	Glu	Asp	Ile	Thr	Leu	His	Asn	Gly	Ser	Val	Ile	Ser	Gly
1865						1870					1875			
Asn	Asn	Val	Gln	Leu	Ala	Gly	Gly	Asn	Ile	Thr	Asn	Ser	Gly	Gly
1880						1885					1890			
Ser	Ile	Asn	Ala	Gln	Asn	Asp	Leu	Ser	Leu	Asp	Ser	Ser	Gly	Tyr
1895						1900					1905			
Ile	Asp	Asn	Leu	Asn	Ala	Gly	Leu	Ile	Ser	Ala	Gly	Gly	Ser	Leu
1910						1915					1920			
Asp	Leu	Ser	Ala	Ile	Gly	Asp	Ile	Ser	Asn	Ile	Ser	Ser	Val	Ile
1925						1930					1935			
Ser	Gly	Lys	Thr	Val	Gln	Leu	Glu	Ser	Val	Ser	Gly	Asn	Ile	Ser
1940						1945					1950			
Asn	Ile	Thr	Arg	Arg	Gln	Gln	Trp	Asn	Ala	Gly	Ser	Asp	Ser	Gln
1955						1960					1965			
Tyr	Gly	Gly	Val	His	Leu	Ser	Gly	Thr	Asp	Thr	Gly	Pro	Val	Ala
1970						1975					1980			
Thr	Ile	Lys	Gly	Thr	Asp	Ser	Leu	Ser	Leu	Asp	Ala	Gly	Lys	Asn
1985						1990					1995			

Ile Asp 2000	Ile Thr Gly Ala Thr 2005	Val Ser Ser Gly Gly 2010	Asp Leu Gly
Met Ser 2015	Ala Gly Asn Asp Ile 2020	Asn Ile Ala Ala Asn 2025	Leu Ile Ser
Gly Ser 2030	Lys Ser Gln Ser Gly 2035	Phe Trp His Thr Asp 2040	Asp Asn Ser
Ser Ser 2045	Ser Thr Thr Ser Gln 2050	Gly Ser Ser Ile Ser 2055	Ala Gly Gly
Asn Leu 2060	Ala Met Ala Ala Gly 2065	His Asn Leu Asp Val 2070	Thr Ala Ser
Ser Val 2075	Ser Ala Gly His Ser 2080	Ala Leu Leu Ser Ala 2085	Gly Asn Asp
Leu Ser 2090	Leu Asn Ala Val Arg 2095	Glu Ser Lys Asn Ser 2100	Arg Asn Gly
Arg Ser 2105	Glu Ser His Glu Ser 2110	His Ala Ala Val Ser 2115	Thr Val Thr
Ala Gly 2120	Asp Asn Phe Leu Leu 2125	Val Ala Gly Arg Asp 2130	Ile Ala Ser
Gln Ala 2135	Ala Gly Met Ala Ala 2140	Glu Asn Asn Val Val 2145	Ile Arg Gly
Gly Arg 2150	Asp Val Asn Leu Val 2155	Ala Glu Ser Ala Gly 2160	Ala Gly Asp
Ser Tyr 2165	Thr Ser Lys Lys Lys 2170	Lys Glu Ile Asn Glu 2175	Thr Val Arg
Gln Gln 2180	Gly Thr Glu Ile Ala 2185	Ser Gly Gly Asp Thr 2190	Thr Val Asn
Ala Gly 2195	Arg Asp Ile Thr Ala 2200	Val Ala Ser Ser Val 2205	Thr Ala Thr
Gly Asn 2210	Ile Ser Val Asn Ala 2215	Gly Arg Asp Val Ala 2220	Leu Thr Thr

Ala	Thr	Glu	Ser	Asp	Tyr	His	Tyr	Leu	Glu	Thr	Lys	Lys	Lys	Ser
2225						2230					2235			
Gly	Gly	Phe	Leu	Ser	Lys	Lys	Thr	Thr	Arg	Thr	Ile	Ser	Glu	Asp
2240						2245					2250			
Ser	Ala	Thr	Arg	Glu	Ala	Gly	Ser	Leu	Leu	Ser	Gly	Asn	Arg	Val
2255						2260					2265			
Thr	Val	Asn	Ala	Gly	Asp	Asn	Leu	Thr	Val	Glu	Gly	Ser	Asp	Val
2270						2275					2280			
Val	Ala	Asp	Arg	Asp	Val	Ser	Leu	Ala	Ala	Gly	Asn	His	Val	Asp
2285						2290					2295			
Val	Leu	Ala	Ala	Thr	Ser	Thr	Asp	Thr	Ser	Trp	Arg	Phe	Lys	Glu
2300						2305					2310			
Thr	Lys	Lys	Ser	Gly	Leu	Met	Gly	Thr	Gly	Gly	Ile	Gly	Phe	Thr
2315						2320					2325			
Ile	Gly	Ser	Ser	Lys	Thr	Thr	His	Asp	Arg	Arg	Glu	Ala	Gly	Thr
2330						2335					2340			
Thr	Gln	Ser	Gln	Ser	Ala	Ser	Thr	Ile	Gly	Ser	Thr	Ala	Gly	Asn
2345						2350					2355			
Val	Ser	Ile	Thr	Ala	Gly	Lys	Gln	Ala	His	Ile	Ser	Gly	Ser	Asp
2360						2365					2370			
Val	Ile	Ala	Asn	Arg	Asp	Ile	Ser	Ile	Thr	Gly	Asp	Ser	Val	Val
2375						2380					2385			
Val	Asp	Pro	Gly	His	Asp	Arg	Arg	Thr	Val	Asp	Glu	Lys	Phe	Glu
2390						2395					2400			
Gln	Lys	Lys	Ser	Gly	Leu	Thr	Val	Ala	Leu	Ser	Gly	Thr	Val	Gly
2405						2410					2415			
Ser	Ala	Ile	Asn	Asn	Ala	Val	Thr	Ser	Ala	Gln	Glu	Thr	Lys	Glu
2420						2425					2430			
Ser	Ser	Asp	Ser	Arg	Leu	Lys	Ala	Leu	Gln	Ala	Thr	Lys	Thr	Ala
2435						2440					2445			

Leu Ser Gly Val Gln Ala Gly Gln Ala Ala Thr Met Ala Ser Ala
2450 2455 2460

Thr Gly Asp Pro Asn Ala Met Gly Val Ser Leu Ser Leu Thr Thr
2465 2470 2475

Gln Lys Ser Lys Ser Gln Gln His Ser Glu Ser Asp Thr Val Ser
2480 2485 2490

Gly Ser Thr Leu Asn Ala Gly Asn Asn Leu Ser Val Val Ala Thr
2495 2500 2505

Gly Lys Asn Arg Gly Asp Asn Arg Gly Asp Ile Val Ile Ala Gly
2510 2515 2520

Ser Gln Leu Lys Ala Gly Gly Asn Thr Ser Leu Asp Ala Ala Asn
2525 2530 2535

Asp Ile Leu Leu Ser Gly Ala Ala Asn Thr Gln Lys Thr Thr Gly
2540 2545 2550

Arg Asn Ser Ser Ser Gly Gly Gly Val Gly Val Ser Ile Gly Ala
2555 2560 2565

Gly Gly Asn Gly Ala Gly Ile Ser Val Phe Ala Gly Val Asn Ala
2570 2575 2580

Ala Lys Gly Ser Glu Lys Gly Asn Gly Thr Glu Trp Thr Glu Thr
2585 2590 2595

Thr Thr Asp Ser Gly Lys Thr Val Thr Ile Asn Ser Gly Arg Asp
2600 2605 2610

Thr Val Leu Asn Gly Ala Gln Val Asn Gly Asn Arg Ile Ile Ala
2615 2620 2625

Asp Val Gly His Asp Leu Leu Ile Ser Ser Gln Gln Asp Thr Ser
2630 2635 2640

Lys Tyr Asp Ser Lys Gln Thr Ser Val Ala Ala Gly Gly Ser Phe
2645 2650 2655

Thr Phe Gly Ser Met Thr Gly Ser Gly Tyr Ile Ala Ala Ser Arg
2660 2665 2670

Asp Lys Met Lys Ser Arg Phe Asp Ser Val Ala Glu Gln Thr Gly
2675 2680 2685

Met Phe Ala Gly Asp Gly Gly Phe Asp Ile Thr Val Gly Arg His
2690 2695 2700

Thr Gln Leu Asp Gly Ala Val Ile Ala Ser Thr Ala Thr Pro Asp
2705 2710 2715

Lys Asn His Leu Asp Thr Gly Thr Leu Gly Phe Ser Asp Leu His
2720 2725 2730

Asn Glu Ala Asp Tyr Lys Val Ser His Ser Gly Ile Ser Leu Ser
2735 2740 2745

Gly Gly Gly Ser Phe Gly Asp Lys Phe Gln Gly Asn Met Pro Gly
2750 2755 2760

Gly Met Ile Ser Ala Gly Gly His Ser Gly His Ala Glu Gly Thr
2765 2770 2775

Thr Gln Ala Ala Val Ala Glu Gly Thr Ile Thr Ile Arg Asp Arg
2780 2785 2790

Asp Asn Gln Lys Gln Asn Leu Ala Asn Leu Ser Arg Asp Pro Ala
2795 2800 2805

His Ala Asn Asp Ser Ile Ser Pro Ile Phe Asp Lys Glu Lys Glu
2810 2815 2820

Gln Arg Arg Leu Gln Thr Val Gly Leu Ile Lys
2825 2830

<210> 253
<211> 1539
<212> PRT
<213> Escherichia coli

<220>
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<222> (1531)..(1531)
<223> The 'Xaa' at location 1531 stands for Thr.

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<222> (13480)..(13480)
<223> Unsure

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<400> 253

Met Lys Met Ile Phe Thr Gly Lys Val Ser Gly Glu Lys Thr Val Leu
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Thr Val Gly Gly Arg His Thr Val Lys Ala Gln Pro Gly Glu Gln Tyr
20 25 30

Gly Leu Ile Asp Glu Val Thr Gly Leu Val Pro Asp Gly Val Glu Ala
35 40 45

Asp Arg Ser Gly Asp Asp Leu Ile Leu Arg Lys Lys Glu Glu Asp Thr
50 55 60

Glu Val Arg Ile Glu Gly Phe Trp Glu Glu Cys Gln Pro Gly Glu Thr
65 70 75 80

Gln Cys Thr Ala Val Phe Asn Ile Val Gly Glu Asp Gly Gln Val Thr
85 90 95

Glu Ala Val Leu Thr Gln Asp Gly Pro Val Leu Asp Asp Ile Thr Ala
100 105 110

Gly Gln Ser Gly Thr Leu Ser Asp Asp Asp Arg Gly Gly Phe Ile Trp
115 120 125

Leu Gly Gly Leu Ala Phe Gly Gly Gly Leu Ala Ala Met Ala Leu Ala
130 135 140

Ala Gly Gly Gly Gly Ser Lys His Arg His Glu Asn Asp Asp Ser Asp
145 150 155 160

Thr Thr Ala Pro Ser Ser Pro Ala Leu Lys Ala Glu Asp Asp Gly Ser
165 170 175

Val Ser Val Glu Leu Pro Gly Asp Ala Asn Lys Gly Asp Thr Val Asp
180 185 190

Val Thr Phe Glu Asp Glu Lys Gly Gly Lys His Thr Val Thr Leu Glu
195 200 205

Lys Gly Asp Asn Gly Trp Thr Ser Ser Asp Pro Thr Leu Ile Pro Asp
210 215 220

Ser Thr Gly Asp Lys Ala Thr Ile Pro Ala Asp Asn Val Lys Asp Asn
225 230 235 240

Ser Glu Val Thr Gly Val Ala Lys Asp Pro Ser Gly Asn Glu Ser Asp
245 250 255

Pro Ser Thr Val Thr Ser Lys Thr Asp Gly Val Ala Asp Ala Pro Val
260 265 270

Leu Ser Ile Pro Glu Val Thr Asp Gly Tyr Ala Asn Ala Asp Glu Leu
275 280 285

Lys Asp Gly Leu Gln Ala Glu Val Thr Leu Pro Ala Gly Thr Ala Glu
290 295 300

Gly Ala Val Ile Thr Leu Thr Val Thr Arg Pro Asp Lys Thr Thr Glu
305 310 315 320

Asn Val Thr His Thr Val Thr Lys Asp Glu Val Ala Ala Gly Lys Val
325 330 335

Ser Met Asp Ile Pro Lys Asp Ala Val Ile Asp Gly Gln Asn Ser Val
340 345 350

Ser Val Thr Leu Thr Gln Gly Ser Asn Pro Ala Lys Pro Gly Asn Val
355 360 365

Val Asp Phe Ala Ala Asp Thr Gln Ile Pro Gly Asp Thr Asp Gly Asp
370 375 380

Gly Ala Thr Asp Ala Thr Pro Val Val Ala Ile Pro Glu Ala Ala Asp
385 390 395 400

Gly Val Asn Ala Glu Glu Leu Lys Asp Gly Val Gln Thr Glu Val Thr
405 410 415

Val Pro Lys Gly Ser Ala Ala Gly Asp Thr Leu Thr Leu Thr Val Thr
420 425 430

Lys Pro Asp Gly Thr Thr Asp Thr Val Glu His Thr Leu Thr Ala Asp
435 440 445

Glu Val Ala Ala Gly Lys Ala Asp Val Thr Ile Pro Ala Asp Lys Val
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Ser Thr Val Thr Ser Lys Thr Asp Gly Val Ala Asp Ala Pro Val Leu
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Ala Asp Gly Gln Tyr Ser Val Thr Ala Glu Ile Thr Asp Pro Ala Gly
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Trp Val Gln Lys Asp Ser Ser Gly Thr Ala Asn Ser Glu Ile Ile Asn
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